

In the United States Patent and Trademark Office

In re the application of:)	
Jagir Razak Jainul)	
Abdeen Hussan)	
)	
Filed: 10/31/2003)	Group Art Unit: 1631
)	
For: Multisequence Data)	Examiner: Pablo S. Whaley
Representation)	
)	
Application No. 10/699,024)	
)	
Appellant's Docket:)	
JP920030152US1)	

Mail Stop Appeal Brief - Patents
Commissioner of Patents and Trademarks
PO Box 1450
Alexandria, VA 22313-1450

This is an appeal from the Final Rejection of October 7, in which all pending claims were rejected.

REAL PARTY IN INTEREST

The assignee, International Business Machines Corporation, is the real party in interest.

RELATED APPEALS AND INTERFERENCES

This is the first appeal in the present patent application. There are no other appeals or interferences known to the appellant or its legal representative. International Business Machines Corporation is the sole assignee of the patent application.

STATUS OF CLAIMS

Claims 3-6, 10, 14-22, and 24-38 are pending in the application and stand rejected.

Claims 1, 2, 7-9, 11-13, and 23 were previously canceled.

The claims appealed herein are claims 14, 24, and 27.

The present application was filed on October 31, 2003. Claims 1-13 were originally presented. An Office action of August 15, 2007 presented a restriction requirement. Appellant traversed the restriction requirement in a response of September 17, 2007. In the same response, Appellant also amended all claims in order to more certainly ensure that the claims were directed to a single invention, to provide sufficient antecedent basis for all terms, and to properly format the claims.

A first Office action of December 12, 2007, rejected claims 1-13 under 35 USC 112, second paragraph, claims 1-13 under 35 USC 101, and claims 1-13 under 35 USC 103(a) as being unpatentable over Computer and Chemistry, 1999, Vol. 23, p. 365-385 ("Taylor"), in view of US 5,832,272 ("Kalantery").

In Reply A of March 11, 2008, Appellant canceled claims 12-13, amended claims, 1, 2, and 3-6 to overcome the 112, second paragraph rejection, amended claim 1 to overcome the 101 rejection, and amended claim 1 and its dependent claims to overcome the 103 rejection.

A final Office action of July 9, 2008, objected to the specification, rejected claims 2-11 under 35 USC 101, and rejected claims 1-11 under 35 USC 103(a) as being unpatentable over Taylor in view of Kalanter, and in view of Proteins: Structure, Function, and Genetics, 1991, Vol. 11, p. 59-76 ("Huysmans").

In an amendment accompanying a Request for Continued Examination of October 8, 2008, Appellant amended the specification to overcome the objection, amended claims 2-11 and traversed to overcome the 101 rejection, canceled claim 1, and added claims 14-23 to overcome the 103(a) rejection.

A nonfinal rejection of February 10, 2009 objected to the specification, rejected claims 3-6, 10, 14-23 under 35 USC 101, and rejected all pending claims under 35 USC 103(a).

In an amendment filed May 11, 2009, Appellant responsively amended the specification, amended independent claim 14, amended dependent claims 4, 5, 6, 15, 17, 19, 21 and 22, and canceled claim 23 to overcome the objections and rejections.

A final rejection of August 4, 2009, withdrew all previous rejections and newly rejected claim 14 under 35 USC 112, first and second paragraphs, newly rejected claims 4, 5 and 14-22 under 35 USC 103(a) as being unpatentable over Taylor et al., Computer and Chemistry, 1999, Vol. 23, p. 365-385 ("Taylor"), in view of Chen et al., Bioinformatics, 2002, Vol. 18, No. 12, p. 1696-1698 ("Chen"), and further in view of Schwartz et al., Genome Research, 2000, Vol. 10, p. 577-586 ("Schwartz"), newly rejected claims 3-6 and 10 under 35 USC 103(a) as being unpatentable over Taylor, in view of Chen, in view of Schwartz, and further in view of Huysmans et al., Proteins: Structure, Function, and Genetics, 1991, Vol. 11, p. 59-76 ("Huysmans").

In an amendment accompanying a Request for Continued Examination of November 4, 2009, Appellant amended claims 4-6, 10, and 14 to overcome the rejections. In a supplemental amendment of November 19, 2009, Appellant added computer program product and computer system claims previously canceled merely to facilitate expeditious prosecution of the remaining claims.

A nonfinal, Office Action of February 2, 2010, withdrew the rejection of claims 3-6, 10, 14-22 under 35 U.S.C. 112, second paragraph, rejected claims 3-6, 10, 14-

22, 24-28 under 35 U.S.C. 112, first paragraph, newly rejected claims 3-6, 10, 14-22, 24-28 under 35 U.S.C. 112, second paragraph, and rejected claims 4, 5, 14-22, 24, 27, and 28 under 35 U.S.C. 103(a) as being unpatentable over Rigoustos et al. (Bioinformatics, 1998, Vol. 14, No. 1, p. 55-67), in view of Chen, in view of Orcutt et al. (Nucleic Acids Research, 1982, Vol. 10, No. 1, p. 157-174), in view of Zhang et al. (Genome Research, 1997, Vol. 7, p. 649-656), and in view of UK CROPNETT ([http://ukcrop.net/agr/sequence display key#sequence](http://ukcrop.net/agr/sequence%20display%20key%20sequence); Published 200 1, p. 1-5).

In an Reply to Nonfinal Office Action of May 3, 2010, Appellant traversed Examiner's rejections and amended claims 5, 6, 10, 14, 15, 17, 19, 24, 26, and 27 to overcome the 35 U.S.C. 112, first and second paragraph overcome the 35 U.S.C. 103(a) rejections.

The present, final Office action of October 7, 2010, withdrew the rejection of claims 3-6, 10, 14-22, 24-28 under 35 U.S.C. 112 first paragraph, and maintained the rejection of claims 3-6, 10, 14-22 under 35 U.S.C. 112, second paragraph and the rejection of claims 4, 5, 14-22, 24, 27, and 28 under 35 U.S.C. 103(a) as being unpatentable over Rigoutsos et al. (Bioinformatics, 1998, Vol. 14, No. 1, p. 55-67), in view of Chen, in view of Orcutt et al. (Nucleic Acids Research, 1982, Vol. 10, No. 1, p. 157-174), in view of Zhang et al. (Genome Research, 1997, Vol. 7, p. 649-656), and in view of UK CROPNETT ([http://ukcrop.net/agr/sequence display key#sequence](http://ukcrop.net/agr/sequence%20display%20key%20sequence); Published 200 1, p. 1-5).

STATUS OF AMENDMENTS

There are no amendments in connection with this appeal. All amendments that have been submitted have been entered. The claims in the Claim Appendix herein set out the claims that are the subject of the appeal.

SUMMARY OF CLAIMED SUBJECT MATTER

The present application discloses methods, systems, and computer program products for storing and presenting sequence data.

Claim 14

Claim 14 describes a computer system-implemented method for storing and presenting sequence data. The claim includes steps, as follows:

Step: specifying a set of replets for analysis by a computer system;

Step: for each replet in the set, comparing each replet by the computer system to a sequence for determining by the computer system a subsequence of the sequence that matches each replet, if any, wherein the sequence represents a genome sequence;

Step: generating, by the computer system responsive to the comparing, respective entries of a match-set data structure, the match-set data structure having respective entries for the respective replets, each entry comprising a sequence identification to identify a sequence where a match occurs and offset information to determine a position within the sequence where the matching subsequence of the sequence is located, wherein the offset information comprises a first and second position parameter;

Step: storing the generated entries of the match-set data structures in a computer readable memory by the computer system;

Step: deleting by the computer system each matching subsequence from the sequence where it is found;

Step: concatenating by the computer system, in order, unmatched regions of sequences that remain after deleting each matching subsequence to form and store a backbone sequence;

Step: the computer system generating or receiving a selection of at least a first one of the replets, wherein at least a portion of one of the matching subsequences is matched by a certain plurality of the replets and the received selection includes a selection of at least one of the certain plurality of replets;

Step: the computer system generating a first instance of the sequence and presenting the first instance of the sequence to a user of the computer system, wherein the generating of the sequence is responsive to the stored backbone sequence and responsive to the at least one of the stored match-set data entries corresponding to the selected at least first one of the replets, wherein the first position parameter of each match-set data structure entry denotes a location in the sequence and the second position parameter of each match-set data structure entry denotes an offset from the location, wherein the selected at least first one of the replets has a position within the sequence, and wherein after receiving the selection the computer system updates the first and second parameters of the entries in the match-set data structure, the updating being responsive to the position of the selected at least first one of the replets;

Step: the computer system generating or receiving a selection of a second one of the replets; and

Step: the computer system generating and presenting a second instance of the sequence to a user responsive to the at least second one of the replets and wherein the computer system performs the generating of the second instance of the sequence by reference to the updated first and second parameters for the second one of the replets.

The specification describes the method of claim 14 in terms of an embodiment of the invention. Specifically, regarding support for claim 14, see application as filed page 2, lines 26-27 (A computer system-implemented method for storing and presenting sequence data, comprising); page 2, lines 19-20, page 8, lines 21-25, and page 9, lines 1-5 (specifying a set of replets for analysis by a computer system, for each replet in the set, comparing each replet by the computer system to a sequence for determining by the computer system a subsequence of the sequence that matches each replet, if any, wherein the sequence represents a genome sequence); page 9, line 27-30 and page 10, lines 9-17 (generating, by the computer system responsive to the comparing, respective entries of a match-set data structure, the match-set data structure having respective entries for the respective replets, each

entry comprising a sequence identification to identify a sequence where a match occurs and offset information to determine a position within the sequence where the matching subsequence of the sequence is located); Fig. 3, page 10, lines 15-25 (wherein the offset information comprises a first and second position parameter); page 10, line 31, page 20, lines 5-10 (storing the generated entries of the match-set data structures in a computer readable memory by the computer system); page 9, lines 1-2 (deleting by the computer system each matching subsequence from the sequence where it is found); page 9, lines 21-25 (concatenating by the computer system, in order, unmatched regions of sequences that remain after deleting each matching subsequence to form and store a backbone sequence); page 4, lines 9-29; page 8, lines 27-32 (the computer system generating or receiving a selection of at least a first one of the replets); 10, lines 1-3 (wherein at least a portion of one of the matching subsequences is matched by a certain plurality of the replets and the received selection includes a selection of at least one of the certain plurality of replets); page 10, lines 1-3 and page 21, lines 14-16 (the computer system generating a first instance of the sequence and presenting the first instance of the sequence to a user of the computer system, wherein the generating of the sequence is responsive to the stored backbone sequence and responsive to the at least one of the stored match-set data entries corresponding to the selected at least first one of the replet); Fig. 3, page 10, lines 15-25 (wherein the first position parameter of each match-set data structure entry denotes a location in the sequence and the second position parameter of each match-set data structure entry denotes an offset from the location); page 10, lines 5-13 (wherein the selected at least first one of the replets has a position within the sequence, and wherein after receiving the selection the computer system updates the first and second parameters of the entries in the match-set data structure, the updating being responsive to the position of the selected at least first one of the replets); Page 12, line 30-page 13, line 6 (the computer system generating or receiving a selection of a second one of the replets and the computer system generating and presenting a second instance of the sequence to a user responsive to the at least second one of the replets); page 14, lines 10-15 (and wherein the computer system performs the generating of the second

instance of the sequence by reference to the updated first and second parameters for the second one of the replets).

Claim 24

Claim 24, describes a computer program product, for storing and presenting sequence data, the computer program product including a computer readable storage medium having instructions stored thereon for execution by a computer, wherein the instructions, when executed by the computer, cause the computer to implement a method. The claim includes steps, as follows:

Step: specifying a set of replets for analysis by a computer system;

Step: each replet in the set, comparing each replet by the computer system to a sequence for determining by the computer system a subsequence of the sequence that matches each replet, if any, wherein the sequence represents a genome sequence;

Step: generating, by the computer system responsive to the comparing, respective entries of a match-set data structure, the match-set data structure having respective entries for the respective replets, each entry comprising a sequence identification to identify a sequence where a match occurs and offset information to determine a position within the sequence where the matching subsequence of the sequence is located, wherein the offset information comprises a first and second position parameter,;

Step: storing the generated entries of the match-set data structures in a computer readable memory by the computer system;

Step: deleting by the computer system each matching subsequence from the sequence where it is found;

Step: concatenating by the computer system, in order, unmatched regions of sequences that remain after deleting each matching subsequence to form and store a backbone sequence;

Step: the computer system generating or receiving a selection of at least a first one of the replets, wherein at least a portion of one of the matching

subsequences is matched by a certain plurality of the replets and the received selection includes a selection of at least one of the certain plurality of replets;

Step: the computer system generating a first instance of the sequence and presenting the first instance of the sequence to a user of the computer system, wherein the generating of the sequence is responsive to the stored backbone sequence and responsive to the at least one of the stored match-set data entries corresponding to the selected at least first one of the replet, wherein the first position parameter of each match-set data structure entry denotes a location in the sequence and the second position parameter of each match-set data structure entry denotes an offset from the location, wherein the selected at least first one of the replets has a position within the sequence, and wherein after receiving the selection the computer system updates the first and second parameters of the entries in the match-set data structure, the updating being responsive to the position of the selected at least first one of the replets;

Step: the computer system generating or receiving a selection of a second one of the replets; and

Step: the computer system generating and presenting a second instance of the sequence to a user responsive to the at least second one of the replets and wherein the computer system performs the generating of the second instance of the sequence by reference to the updated first and second parameters for the second one of the replets.

The specification describes the computer program product of claim 24 in terms of an embodiment of the invention. Specifically, regarding support for claim 24, see application as filed page 20, lines 5-10 and page 2, lines 26-27 (computer program product for storing and presenting sequence data, the computer program product including a computer readable storage medium having instructions stored thereon for execution by a computer, wherein the instructions, when executed by the computer, cause the computer to implement a method); page 2, lines 19-20, page 8, lines 21-25, and page 9, lines 1-5 (specifying a set of replets for analysis by a computer system, for each replet in the set, comparing each replet by the computer system to a

sequence for determining by the computer system a subsequence of the sequence that matches each replet, if any, wherein the sequence represents a genome sequence); page 9, line 27-30 and page 10, lines 9-17 (generating, by the computer system responsive to the comparing, respective entries of a match-set data structure, the match-set data structure having respective entries for the respective reptlets, each entry comprising a sequence identification to identify a sequence where a match occurs and offset information to determine a position within the sequence where the matching subsequence of the sequence is located); Fig. 3, page 10, lines 15-25 (wherein the offset information comprises a first and second position parameter); page 10, line 31, page 20, lines 5-10 (storing the generated entries of the match-set data structures in a computer readable memory by the computer system); page 9, lines 1-2 (deleting by the computer system each matching subsequence from the sequence where it is found); page 9, lines 21-25 (concatenating by the computer system, in order, unmatched regions of sequences that remain after deleting each matching subsequence to form and store a backbone sequence); page 4, lines 9-29; page 8, lines 27-32 (the computer system generating or receiving a selection of at least a first one of the reptlets); 10, lines 1-3 (wherein at least a portion of one of the matching subsequences is matched by a certain plurality of the reptlets and the received selection includes a selection of at least one of the certain plurality of reptlets); page 10, lines 1-3 and page 21, lines 14-16 (the computer system generating a first instance of the sequence and presenting the first instance of the sequence to a user of the computer system, wherein the generating of the sequence is responsive to the stored backbone sequence and responsive to the at least one of the stored match-set data entries corresponding to the selected at least first one of the reptlet); Fig. 3, page 10, lines 15-25 (wherein the first position parameter of each match-set data structure entry denotes a location in the sequence and the second position parameter of each match-set data structure entry denotes an offset from the location); page 10, lines 5-13 (wherein the selected at least first one of the reptlets has a position within the sequence, and wherein after receiving the selection the computer system updates the first and second parameters of the entries in the match-set data structure, the updating being responsive to the position of the

selected at least first one of the replets); Page 12, line 30-page 13, line 6 (the computer system generating or receiving a selection of a second one of the replets and the computer system generating and presenting a second instance of the sequence to a user responsive to the at least second one of the replets); page 14, lines 10-15 (and wherein the computer system performs the generating of the second instance of the sequence by reference to the updated first and second parameters for the second one of the replets).

Claim 27

Claim 27, describes a computer system comprising a processor and a storage device connected to the processor, wherein the storage device has stored thereon data storage reducing program for controlling the processor, and wherein the processor is operative to execute instructions of the program to implement a method. The claim includes steps, as follows:

Step: specifying a set of replets for analysis by a computer system;

Step: for each replet in the set, comparing each replet by the computer system to a sequence for determining by the computer system a subsequence of the sequence that matches each replet, if any, wherein the sequence represents a genome sequence;

Step: generating, by the computer system responsive to the comparing, respective entries of a match-set data structure, the match-set data structure having respective entries for the respective replets, each entry comprising a sequence identification to identify a subsequence where a match occurs and offset information to determine a position within the sequence where the matching subsequence of the sequence is located, wherein the offset information comprises a first and second position parameter,;

Step: storing the generated entries of the match-set data structures in a computer readable memory by the computer system;

Step: deleting by the computer system each matching subsequence from the sequence where it is found;

Step: concatenating by the computer system, in order, unmatched regions of sequences that remain after deleting each matching subsequence to form and store a backbone sequence;

Step: the computer system generating or receiving a selection of at least a first one of the replets, wherein at least a portion of one of the matching subsequences is matched by a certain plurality of the replets and the received selection includes a selection of at least one of the certain plurality of replets;

Step: the computer system generating a first instance of the sequence and presenting the first instance of a the sequence to a user of the computer, wherein the generating of the sequence is responsive to the stored backbone sequence and responsive to the at least one of the stored match-set data entries corresponding to the selected at least first one of the replets, wherein the first position parameter of each match-set data structure entry denotes a location in the sequence and the second position parameter of each match-set data structure entry denotes an offset from the location, wherein the selected at least first one of the replets has a position within the sequence, and wherein after receiving the selection the computer system updates the first and second parameters of the entries in the match-set data structure, the updating being responsive to the position of the selected at least first one of the replets;

Step: the computer system generating or receiving a selection of a second one of the replets; and

Step: the computer system generating and presenting a second instance of the sequence to a user responsive to the at least second one of the replets and wherein the computer system performs the generating of the second instance of the sequence by reference to the updated first and second parameters for the second one of the replets.

The specification describes the computer program product of claim 27 in terms of an embodiment of the invention. Specifically, regarding support for claim 27, see application as filed page 19, lines 4-31 and page 2, lines 26-27 (A computer system comprising a processor; and a storage device connected to the processor, wherein

the storage device has stored thereon a program for controlling the processor, and wherein the processor is operative with the program to execute the program for performing the steps of); page 2, lines 19-20, page 8, lines 21-25, and page 9, lines 1-5 (specifying a set of replets for analysis by a computer system, for each replet in the set, comparing each replet by the computer system to a sequence for determining by the computer system a subsequence of the sequence that matches each replet, if any, wherein the sequence represents a genome sequence); page 9, line 27-30 and page 10, lines 9-17 (generating, by the computer system responsive to the comparing, respective entries of a match-set data structure, the match-set data structure having respective entries for the respective replets, each entry comprising a sequence identification to identify a sequence where a match occurs and offset information to determine a position within the sequence where the matching subsequence of the sequence is located); Fig. 3, page 10, lines 15-25 (wherein the offset information comprises a first and second position parameter); page 10, line 31, page 20, lines 5-10 (storing the generated entries of the match-set data structures in a computer readable memory by the computer system); page 9, lines 1-2 (deleting by the computer system each matching subsequence from the sequence where it is found); page 9, lines 21-25 (concatenating by the computer system, in order, unmatched regions of sequences that remain after deleting each matching subsequence to form and store a backbone sequence); page 4, lines 9-29; page 8, lines 27-32 (the computer system generating or receiving a selection of at least a first one of the replets); 10, lines 1-3 (wherein at least a portion of one of the matching subsequences is matched by a certain plurality of the replets and the received selection includes a selection of at least one of the certain plurality of replets); page 10, lines 1-3 and page 21, lines 14-16 (the computer system generating a first instance of the sequence and presenting the first instance of the sequence to a user of the computer system, wherein the generating of the sequence is responsive to the stored backbone sequence and responsive to the at least one of the stored match-set data entries corresponding to the selected at least first one of the replet); Fig. 3, page 10, lines 15-25 (wherein the first position parameter of each match-set data structure entry denotes a location in the sequence and the second position parameter

of each match-set data structure entry denotes an offset from the location); page 10, lines 5-13 (wherein the selected at least first one of the replets has a position within the sequence, and wherein after receiving the selection the computer system updates the first and second parameters of the entries in the match-set data structure, the updating being responsive to the position of the selected at least first one of the replets); Page 12, line 30-page 13, line 6 (the computer system generating or receiving a selection of a second one of the replets and the computer system generating and presenting a second instance of the sequence to a user responsive to the at least second one of the replets); page 14, lines 10-15 (and wherein the computer system performs the generating of the second instance of the sequence by reference to the updated first and second parameters for the second one of the replets).

GROUND OF REJECTION TO BE REVIEWED ON APPEAL

1. Is the rejection in the Final Office Action proper, wherein claims 14, 24, and 27 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which Appellant regards as the invention?

2. Is the rejection in the Final Office Action proper, wherein claims 14, 24, and 27 are rejected under 35 U.S.C. 103(a) as being unpatentable over Rigoutsos et al. (Bioinformatics, 1998, Vol. 14, No. 1, p. 55-67), in view of Chen et al. (Bioinformatics, 2002, Vol. 18, No. 12, p. 1696-1698), in view of Orcutt et al. (Nucleic Acids Research, 1982, Vol. 10, No. 1, p. 157-174), in view of Zhang et al. (Genome Research, 1997, Vol. 7, p. 649-656), and in view of UK CROPNETT (<http://ukcrop.net/agr/sequence~display~key#sequence>: Published 2001, p. 1-5)?

ARGUMENTS

Appellant herein argues as a group claims 14, 24, and 27.

Claims 3-6, 10, 15-22, 25-26, and 28 stand or fall with their respective base claims.

1. Rejection of claims 14, 24, and 27 under 35 U.S.C. 112, paragraph 2

Claims 14, 24, and 27 stand rejected under 35 U.S.C. 112, second paragraph.

Appellant respectfully submits that the rejection is improper.

The Office action essentially asserts, without citing any authority, that it is indefinite for a claim to recite one thing is “responsive to” another. More specifically, the rejection states that it is unclear in what way a computer system generates a representation of a sequence that is responsive to a stored backbone sequence and stored match-set data, and in what way updating is responsive to the recited position.

Appellant respectfully disagrees. To make an analogy, it may be said in a mathematical problem that “x is a function of u and v,” for example. While this terminology does not specify an exact formula involving u and v, it does quite definitely indicate that the computation of x requires values for a and b. It provides a definite limitation regarding how x is computed. This is not a matter of indefiniteness, but rather breadth. Breadth of a claim is not to be equated with indefiniteness. MPEP 2173.04 (citing *In re Miller*, 441 F.2d 689, 169 USPQ 597 (CCPA 1971)).

Likewise, the claims provide a definite limitation regarding how a representation is generated by reciting in the claims that a computer system generates a representation responsive to a stored backbone sequence and match-set data. And reciting that updating is responsive to a position provides a definite limitation regarding how the updating is performed.

Further, there is no allegation that the specification fails to also disclose that that a computer system generates a representation responsive to a stored backbone sequence and match-set data or fails to disclose that updating is responsive to a position.

For these reasons, Appellant submits that the rejection is improper.

2. Rejection of claims 14, 24, and 27 under 35 U.S.C. 103(a)

Claims 14, 24, and 27 stand rejected under 35 U.S.C. 103(a) as being unpatentable over Rigoutsos, Chen, Orcutt, Zhang, and in view of UK CROPNETT. Appellant respectfully submits that the rejection is improper.

Claim 14 recites “iii) . . . the match-set data structure having respective entries for the respective replets, each entry comprising a sequence identification to identify a sequence where a match occurs and offset information to determine a position within the sequence where the matching subsequence of the sequence is located, wherein the offset information comprises a first and second position parameter” and “viii) . . . wherein the first position parameter of each match-set data structure entry denotes a location in the sequence and the second position parameter of each match-set data structure entry denotes an offset from the location.” Claims 24 and 27 have similar language.

Claim 14, (viii, further recites “after receiving the selection the computer system updates the first and second parameters of the entries in the match-set data structure , the updating being responsive to the position of the selected at least first one of the replets.”

Appellant has endeavored throughout prosecution of this application to determine what inference and what teaching of which prior art reference is relied upon in each Office action regarding each specific claim limitation. This effort has been impeded by a lack of clarity in the Office actions with regard what specific citations and arguments relate to what specific claim limitations.

The Office action, at page 6, indicates that it relies upon teachings of Rigoutsos regarding comparing each pattern to a sequence for determining a subsequence and generating entries of match-set data structures. Regarding position parameters, the Office action also indicates at page 6 that it relies upon teachings of Rigoutsos regarding “Notation . . . for identifying generated patterns with their associated sequence identification data and offset information [Fig. 1, and p. 56, Col. 2], which shows match-set data having respective entries comprising sequence identification and offset information to determine a position within the sequence. New patterns are constructed based on previous sequences and parameters via an iterative convolution method [p. 58, Col. 1, Fig. 3, p. 59, Col. 1], which shows

generating updated instances of sequence by reference to previous parameters. New offset lists are generated [p. 58, Col. 1].”

The Office action states at page 7 that “Rigoutsos does not teach a first position parameter of each match-set entry denoting a location in the sequence and a second position parameter of each match-set entry denoting an offset position . . .” and states at page 13 that appellant has engaged in attacking the references separately. Nevertheless, the present Office action also immediately thereafter states at page 14 that “Rigoutsos . . . satisfies the claim language for a first and second position parameter,” citing an offset list comprising sequence matches at multiple offset positions, taught by Rigoutsos at p. 56, Col. 2. Further, the Office action specifically cites only teachings of Rigoustos in asserting at page 10 that “it would have been obvious” due to the cited combination of five (5) references “to have updated the first and second parameters of the entries in the match-set data structure to include the position of the selected replets.”¹

While the Office action, page 6, asserts that Rigoutsos, Fig. 1, and p. 56, Col. 2, teaches “Notation . . . for identifying generated patterns with their associated sequence identification data and offset information which shows match-set data having respective entries comprising sequence identification and offset information to determine a position within the sequence,” and while the Office action, page 14, asserts that “an offset list comprising sequence matches at multiple offset positions” is taught by Rigoutsos at p. 56, Col. 2 and that this “satisfies the claim language for a first and second position parameter,” the cited offset list taught by Rigoutsos teaches

¹ At page 14 the Office action acknowledges, in particular, that UK CROPNET is not cited as a teaching for the claim limitation regarding suggest updating first and second parameters after receiving a replet selection, where the updating is responsive to a position of the selected one of the replets. Then the Office action states that “The graphical presentation includes a combination of information including matches to an insert sequence, sequence position, and textual information [See pages 2-3], as set forth above.” Appellant wonders if the Office action is perhaps attempting to suggest that some other arguments presented in the Office action relate to these specific claim limitations, but pages 2-3 of the Office action present only a general allegation and no specific reasoning or specific citation.

a sequence identification and only a single parameter for offset information.

Nowhere does Rigoutsos teach or suggest offset information that “comprises a first and second position parameter . . . wherein the first position parameter of each match-set data structure entry denotes a location in the sequence and the second position parameter of each match-set data structure entry denotes an offset from the location,” as claimed. Nor do any of the five references cited, alone or in combination.

At page 56, col. 2, Rigoutsos teaches a parameter $L_S(P)$, in which “ $\{(i,j) \mid \text{sequence } s_i \text{ matches } P \text{ at offset } j\}$.” Rigoutsos provides a specific example for a set of sequences $S = \{\text{LFAADCHFFEDTR, LKLALCHESEDR, AFAGCHADELFT}\}$, in which parameter L_S applies as follows:

$$L_S(\text{'A.CH. . E'}) = \{(1,4), (2,4), (3,3)\}.$$

In the first set (1,4) of L_S , for example, the “1” is the “sequence s_i ” (i.e., an identifier indicating the first sequence, “LFAADCHFFEDTR”) and the “4” indicates that the string “A.CH. . E” of L_S is found in the first sequence beginning at an offset of 4. Rigoutsos does not teach or suggest that the offset has two parameters.

It does not follow that because Rigoutsos also teaches at p. 58, Col. 1, Fig. 3, and p. 59, Col. 1 about constructing new patterns based on previous sequences and parameters, or about generating updated instances of sequences by reference to previous parameters, or about generating new offset lists, that Rigoutsos teaches or suggests that each match-set entry has both “a sequence identification to identify a sequence where a match occurs and offset information to determine a position within the sequence where the matching subsequence of the sequence is located, wherein the offset information comprises a first and second position parameter,” as claimed, particularly since Rigoutsos does not teach or suggest a first and second position parameter for the offset information. Consequently, the Office action has failed to address all of the limitations in Claims 14, 24 and 27. For at least this reason, the Office action has failed to prove a prima facie case of obviousness in rejecting the claims.

The Office action asserts at page 10 that it would have been obvious due to the cited combination of five references “to have provided a predictable variation of

the display of parameters, such as presenting a first position parameter of each match-set entry denoting a location in the sequence and a second position parameter of each match-set entry denoting an offset position" because "Rigoutsos teaches location and offset parameters and a parameter (Ls) denoting sequence matches at a specific offset; p. 56, Col. 2." The Office action asserts at page 11 that it would have been obvious due to the cited combination of five references "to have updated the first and second parameters of the entries in the match-set data structure to include the position of the selected replets," because "Rigoutsos shows generating new patterns (i.e. replets) and related parameters of position and offset; see p. 58, Col. 1, which suggests updating first and second parameters of match-set data. The motivation would have been to generate a maximal patterns and detected non-maximal patterns with minimal effort, as suggested by Rigoutsos; p. 58, Col. 2." In this regard, the Office action cites *KSR International Co. v. Teleflex Inc* ("KSR").

Appellant submits that these assertions impermissibly substitute conclusory statements for teaching in the prior art and articulated reasoning. In *KSR* the prior art taught all aspects of the claim at issue. See *KSR*, 550 US 398, 413 (2007) ("Asano taught everything contained in claim 4 except the use of a sensor to detect the pedal's position and transmit it to the computer controlling the throttle. That additional aspect was revealed in sources such as the '068 patent and the sensors used by Chevrolet."). When determining whether a claim is obvious, an examiner must make "a searching comparison of the claimed invention - including all its limitations - with the teaching of the prior art." *In re Ochiai*, 71 F.3d 1565, 1572 (Fed. Cir. 1995). Thus, "obviousness requires a suggestion of all limitations in a claim." *CFMT, Inc. v. Yieldup Intern. Corp.*, 349 F.3d 1333, 1342 (Fed. Cir. 2003) (citing *In re Royka*, 490 F.2d 981, 985 (CCPA 1974)). Moreover, "there must be some articulated reasoning with some rational underpinning to support the legal conclusion of obviousness." *KSR*, 127 S. Ct. 1727, 1741 (2007) (quoting *In re Kahn*, 441 F.3d 977, 988 (Fed. Cir. 2006)).

At issue in *KSR* was whether it was proper to require a showing by the "teaching, suggestion or motivation" test ("TSM test") to justify combining the teachings of the references, or else whether the TSM test was properly applied.

KSR, 127 S.Ct. 1727, 1738-39 (2007). The Court indicated justification for combining references does not demand written prior art to the exclusion of common sense. *Id.* But the Court did not go so far as to advocate substituting common sense or assumed common knowledge for written prior art, nor dispense with the requirement that a *prima facie* case of obviousness must show all claim limitations. See *id.* at 1741 (noting that proof of obviousness requires showing each claim element was known in the prior art.)

Although the Office action refers to what it considers to be obvious in view of a combination of the five cited references, Rigoutsos is the only actual prior art teaching cited in the Office action regarding identifying “a sequence identification . . . and offset information to determine a position within the sequence where the matching subsequence of the sequence is located, wherein the offset information comprises a first and second position parameter” and “viii) . . . wherein the first position parameter of each match-set data structure entry denotes a location in the sequence and the second position parameter of each match-set data structure entry denotes an offset from the location,” as claimed. Likewise, Rigoutsos is the only teaching cited in the Office action regarding “after receiving the selection the computer system updates the first and second parameters of the entries in the match-set data structure , the updating being responsive to the position of the selected at least first one of the replets,” as claimed. Rigoutsos simply does not teach or suggest this. Nor do any of the five references cited, alone or in combination.

Regardless of the motivation offered in the present Office action, no reasoned basis is provided for the conclusion that the above recited claim limitations would have been obvious from the combination of five cited references. That is, it does not follow from teaching at p. 56, Col. 2, by Rigoutsos about “location and offset parameters and a parameter (Ls) denoting sequence matches at a specific offset” that it therefore would have been obvious “to have provided a predictable variation of the display of parameters, such as presenting a first position parameter of each match-set entry denoting a location in the sequence and a second position parameter of each match-set entry denoting an offset position.” This is particularly true since

neither Rigoutsos nor the other four cited references teach or suggest how such a second position parameter would be constructed or why it would facilitate providing a predictable variation of the display of parameters, whereas the present application describes these matters.

Regarding the assertion at page 10 of the Office action that it follows from teaching at p. 58, Col. 1, by Rigoutsos about “generating new patterns (i.e. replets) and related parameters of position and offset” that this “suggests updating first and second parameters of match-set data” or that it suggests “updat[ing] the first and second parameters of the entries in the match-set data structure to include the position of the selected replets,” note that this assertion does not clearly relate to the claims. That is, here the Office action does not even clearly assert that Rigoutsos teaches or suggests what is actually claimed, but rather makes an assertion about something that is only vaguely related to what is explicitly and particularly claimed.

Throughout, the Office action generally alleges that the cited references teach or suggest various matters that the Office action does not clearly relate to the exact language of the claim. Even if those matters stated by the Office action are construed to relate to the above recited claim limitations, appellant respectfully submits that these general allegations are too vague to constitute the sort of “substantial reasoning” required for a prima facie case of obviousness, as required under KSR. Further, MPEP 706.02(j) states that “To support the conclusion that the claimed invention is directed to obvious subject matter, either the references must expressly or impliedly suggest the claimed invention or the examiner must present a convincing line of reasoning as to why the artisan would have found the claimed invention to have been obvious in light of the teachings of the references,” This burden has not been met.

In discussion with the Examiner, the suggestion was made that the claims should be further amended to recite how the above claimed feature regarding position parameters enables the advantageous results described in the present application. Appellant respectfully declined.

It is appellant’s position that the disclosure of the specification enables the public to practice the claimed invention. The disclosure shows in great detail how to

implement an invention that includes identifying “a sequence identification . . . and offset information to determine a position within the sequence where the matching subsequence of the sequence is located, wherein the offset information comprises a first and second position parameter” and “viii) . . . wherein the first position parameter of each match-set data structure entry denotes a location in the sequence and the second position parameter of each match-set data structure entry denotes an offset from the location,” and that includes “after receiving the selection the computer system updates the first and second parameters of the entries in the match-set data structure , the updating being responsive to the position of the selected at least first one of the replets,” within the context of the rest of the claim. Unless the Office makes a proper, specific showing that what is explicitly claimed is obvious from the prior art, appellant is entitled to a claim of the recited scope.

For at least the above reasons, Appellant submits that the references cited do not teach or suggest “viii) the computer system generating a first instance of the sequence and presenting the first instance of the sequence to a user of the computer system, wherein the generating of the sequence is responsive to the stored backbone sequence and responsive to the at least one of the stored match-set data entries corresponding to the selected at least first one of the replets, wherein the first position parameter of each match-set data structure entry denotes a location in the sequence and the second position parameter of each match-set data structure entry denotes an offset from the location, wherein the selected at least first one of the replets has a position within the sequence, and wherein after receiving the selection the computer system updates the first and second parameters of the entries in the match-set data structure , the updating being responsive to the position of the selected at least first one of the replets;

ix) the computer system generating or receiving a selection of a second one of the replets; and

x) the computer system generating and presenting a second instance of the sequence to a user responsive to the at least second one of the replets and wherein the computer system performs the generating of the second instance of the sequence by reference to the updated first and second parameters for the second

one of the replets,” as now recited in claim 14. Claims 24 and 27 recite similar language and are similarly distinguishable and allowable over the prior art.

3. Rejection of claims 3-6, 10, 15-22, 25-26, and 28 Under 35 U.S.C. 112, paragraph 2

Claims 3-6, 10, 15-22, and 25-26 are allowable at least because they depend upon allowable base claims.

4. Rejection of claims 3-6, 10, 15-22, 25-26, and 28 Under 35 USC 103(a)

Claims 3-6, 10, 15-22, and 25-26 are allowable at least because they depend upon allowable base claims.

REQUEST FOR ACTION

For the above reasons, Appellant requests that all the pending claims of the present application be allowed and that the application be promptly passed to issuance.

Respectfully submitted,

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Attachments: Claims Appendix, Evidence Appendix, Related Proceedings Appendix

APPENDIX “AA” CLAIMS

1-2. (canceled)

3. (previously presented) The method of claim 14, wherein storing variations is performed using a pointer.

4. (previously presented) The method of claim 14, further comprising, before presenting the represented sequence to a user:
identifying, replets that can be used to represent multiple subsequences.

5. (previously presented) The method of claim 14, further comprising, before presenting the first instance of the sequence to a user:
segmenting the matching subsequences into multiple parts to account for location-specific variations of the matching subsequences in the sequence data.

6. (previously presented) The method of claim 14, further comprising, before presenting the second instance of the sequence to a user:
storing replet information in a replet-information table using a pointer, so that equivalent replet sequences occupy single storage space.

7- 9. (canceled)

10. (previously presented) The method of claim 14, further comprising, before presenting the second instance of the sequence to a user:
storing multiple views of the sequence data at multiple levels of abstraction.

11-13. (canceled)

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14. (previously presented) A computer system-implemented method for storing and presenting sequence data, comprising:

- i) specifying a set of replets for analysis by a computer system;
- ii) for each replet in the set, comparing each replet by the computer system to a sequence for determining by the computer system a subsequence of the sequence that matches each replet, if any, wherein the sequence represents a genome sequence;
- iii) generating, by the computer system responsive to the comparing, respective entries of a match-set data structure, the match-set data structure having respective entries for the respective replets, each entry comprising a sequence identification to identify a sequence where a match occurs and offset information to determine a position within the sequence where the matching subsequence of the sequence is located, wherein the offset information comprises a first and second position parameter;
- iv) storing the generated entries of the match-set data structures in a computer readable memory by the computer system;
- v) deleting by the computer system each matching subsequence from the sequence where it is found;
- vi) concatenating by the computer system, in order, unmatched regions of sequences that remain after deleting each matching subsequence to form and store a backbone sequence;
- vii) the computer system generating or receiving a selection of at least a first one of the replets, wherein at least a portion of one of the matching subsequences is matched by a certain plurality of the replets and the received selection includes a selection of at least one of the certain plurality of replets;
- viii) the computer system generating a first instance of the sequence and presenting the first instance of the sequence to a user of the computer system, wherein the generating of the sequence is responsive to the stored backbone sequence and responsive to the at least one of the stored match-set data entries

APPENDIX “AA” CLAIMS

corresponding to the selected at least first one of the replets, wherein the first position parameter of each match-set data structure entry denotes a location in the sequence and the second position parameter of each match-set data structure entry denotes an offset from the location, wherein the selected at least first one of the replets has a position within the sequence, and wherein after receiving the selection the computer system updates the first and second parameters of the entries in the match-set data structure, the updating being responsive to the position of the selected at least first one of the replets;

ix) the computer system generating or receiving a selection of a second one of the replets; and

x) the computer system generating and presenting a second instance of the sequence to a user responsive to the at least second one of the replets and wherein the computer system performs the generating of the second instance of the sequence by reference to the updated first and second parameters for the second one of the replets.

15. (previously presented) The method of claim 14, wherein, prior to presenting the first instance of the sequence to the user, variations are stored in a list data structure comprising a variation identification.

16. (previously presented) The method of claim 15, wherein the list data structure comprises a subsequence character that matches a “don’t care” character in a replet that matches the subsequence.

17. (previously presented) The method of claim 16, wherein, prior to presenting the first instance of the sequence to the user, the position of the subsequence character within the subsequence is stored in the list data structure.

APPENDIX “AA” CLAIMS

18. (previously presented) The method of claim 15, wherein an indirection pointer points to a variation so that variations common to more than one subsequence are not stored more than once.

19. (previously presented) The method of claim 14, wherein a first instance of the sequence presented to the user is in response to a query by the user.

20. (previously presented) The method of claim 19, wherein a query specifies a replet.

21. (previously presented) The method of claim 14, wherein specifying a set of one or more replets comprises adding a new replet to a pre-existing set for which the steps of claim 14 have been performed.

22. (previously presented) The method of claim 14, wherein specifying a set of one or more replets comprises removing a replet from a pre-existing set for which the steps of claim 14 have been performed.

23. (canceled)

24. (previously presented) A computer program product for storing and presenting sequence data, the computer program product including a computer readable storage medium having instructions stored thereon for execution by a computer, wherein the instructions, when executed by the computer, cause the computer to implement a method comprising the steps of:

- i) specifying a set of replets for analysis by a computer system;
- ii) for each replet in the set, comparing each replet by the computer system to a sequence for determining by the computer system a subsequence of the sequence

APPENDIX “AA” CLAIMS

that matches each replet, if any, wherein the sequence represents a genome sequence;

iii) generating, by the computer system responsive to the comparing, respective entries of a match-set data structure, the match-set data structure having respective entries for the respective reptlets, each entry comprising a sequence identification to identify a sequence where a match occurs and offset information to determine a position within the sequence where the matching subsequence of the sequence is located, wherein the offset information comprises a first and second position parameter,;

iv) storing the generated entries of the match-set data structures in a computer readable memory by the computer system;

v) deleting by the computer system each matching subsequence from the sequence where it is found;

vi) concatenating by the computer system, in order, unmatched regions of sequences that remain after deleting each matching subsequence to form and store a backbone sequence;

vii) the computer system generating or receiving a selection of at least a first one of the reptlets, wherein at least a portion of one of the matching subsequences is matched by a certain plurality of the reptlets and the received selection includes a selection of at least one of the certain plurality of reptlets;

viii) the computer system generating a first instance of the sequence and presenting the first instance of the sequence to a user of the computer system, wherein the generating of the sequence is responsive to the stored backbone sequence and responsive to the at least one of the stored match-set data entries corresponding to the selected at least first one of the reptlet, wherein the first position parameter of each match-set data structure entry denotes a location in the sequence and the second position parameter of each match-set data structure entry denotes an offset from the location, wherein the selected at least first one of the reptlets has a position within the sequence, and wherein after receiving the selection the computer

APPENDIX “AA” CLAIMS

system updates the first and second parameters of the entries in the match-set data structure , the updating being responsive to the position of the selected at least first one of the replets;

ix) the computer system generating or receiving a selection of a second one of the replets; and

x) the computer system generating and presenting a second instance of the sequence to a user responsive to the at least second one of the replets and wherein the computer system performs the generating of the second instance of the sequence by reference to the updated first and second parameters for the second one of the replets .

25. (previously presented) The computer program product of claim 24, wherein storing variations is performed using a pointer.

26. (previously presented) The computer program product of claim 24, further comprising, before presenting the first instance of the sequence to a user: identifying, replets that can be used to represent multiple subsequences.

27. (previously presented) A computer system comprising:

a processor; and

a storage device connected to the processor, wherein the storage device has stored thereon a program for controlling the processor, and wherein the processor is operative with the program to execute the program for performing the steps of:

i) specifying a set of replets for analysis by a computer system;

ii) for each replet in the set, comparing each replet by the computer system to a sequence for determining by the computer system a subsequence of the sequence that matches each replet, if any, wherein the sequence represents a genome sequence;

APPENDIX “AA” CLAIMS

iii) generating, by the computer system responsive to the comparing, respective entries of a match-set data structure, the match-set data structure having respective entries for the respective replets, each entry comprising a sequence identification to identify a subsequence where a match occurs and offset information to determine a position within the sequence where the matching subsequence of the sequence is located, wherein the offset information comprises a first and second position parameter,;

iv) storing the generated entries of the match-set data structures in a computer readable memory by the computer system;

v) deleting by the computer system each matching subsequence from the sequence where it is found;

vi) concatenating by the computer system, in order, unmatched regions of sequences that remain after deleting each matching subsequence to form and store a backbone sequence;

vii) the computer system generating or receiving a selection of at least a first one of the replets, wherein at least a portion of one of the matching subsequences is matched by a certain plurality of the replets and the received selection includes a selection of at least one of the certain plurality of replets;

viii) the computer system generating a first instance of the sequence and presenting the first instance of a the sequence to a user of the computer, wherein the generating of the sequence is responsive to the stored backbone sequence and responsive to the at least one of the stored match-set data entries corresponding to the selected at least first one of the replets, wherein the first position parameter of each match-set data structure entry denotes a location in the sequence and the second position parameter of each match-set data structure entry denotes an offset from the location, wherein the selected at least first one of the replets has a position within the sequence, and wherein after receiving the selection the computer system updates the first and second parameters of the entries in the match-set data structure

APPENDIX “AA” CLAIMS

, the updating being responsive to the position of the selected at least first one of the replets;

ix) the computer system generating or receiving a selection of a second one of the replets; and

x) the computer system generating and presenting a second instance of the sequence to a user responsive to the at least second one of the replets and wherein the computer system performs the generating of the second instance of the sequence by reference to the updated first and second parameters for the second one of the replets.

28. (previously presented) The computer system of claim 27, wherein storing variations is performed using a pointer.

APPENDIX “BB” EVIDENCE

NONE.

APPENDIX “CC” RELATED PROCEEDINGS

NONE.